December 8, 1998

FILE: ARCD:278

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, DC 20231

RE: *U.S. Patent Application Entitled: METHODS FOR IDENTIFYING FACTORS THAT CONTROL THE FOLDING OF AMYLOID PROTEINS OF DIVERSE ORIGIN - Susan Lindquist (Client Ref. UCHI:702)*

Sir:

Transmitted herewith for filing is a 46-page patent specification including 36 claims and an abstract. Also included are Figures 1A-1C, 2A-2D, 3A, 3B, 4A-4D, 5A-5F, 6A-6C, 7A-7D, and 8 on 8 sheets. The specification and drawings constitute the application of Susan Lindquist for the captioned invention.

Please note that this application is filed <u>without</u> an inventor Declaration and Assignment, a Declaration Claiming Small Entity Status, a Power of Attorney, and filing fees. Pursuant to 37 C.F.R. § 1.53(b) and (f), the Applicant requests the Patent and Trademark Office to accept this application and accord a serial number and filing date as of the date this application is deposited with the U.S. Postal Service for Express Mail. Further, the Applicant requests that the NOTICE OF MISSING PARTS-FILING DATE GRANTED pursuant to 37 C.F.R. § 1.53(f) be sent to the undersigned Applicant's representative.

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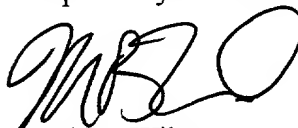
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Please date stamp and return the enclosed postcard to evidence receipt of this application.

Respectfully submitted,

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MBW:plm
Encl.

APPLICATION FOR UNITED STATES LETTERS PATENT

FOR

METHODS FOR IDENTIFYING FACTORS THAT CONTROL THE FOLDING OF

AMYLOID PROTEINS OF DIVERSE ORIGIN

by

SUSAN LINDQUIST

EXPRESS MAIL MAILING LABEL	
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1.0 BACKGROUND OF THE INVENTION

The present application is a continuation of provisional application Serial No. 60/069,168 filed December 9, 1997, and provisional application Serial No. 60/069,168, filed May 8, 1998, the entire disclosure of each of which is incorporated herein by reference without disclaimer. The U.S. government owns rights in the present invention pursuant to grant number NIH GM 25874 from the National Institutes of Health.

1.1 FIELD OF THE INVENTION

The present invention relates generally to the fields of genetics and cellular biology. More particularly, it concerns a yeast based system for the determination of compounds that affect amyloid formation. The present invention relates to the determination of compounds that affect the amyloid associated with Alzheimer's disease, Transmissible spongiform encephalopathies (TSEs), and several rare human neuropathies: Creutzfeld-Jacob disease (CJD), fatal familial insomnia (FFI), Gertsmann-Straussler-Scheinker (GSS) syndrome, and kuru.

1.2 DESCRIPTION OF RELATED ART

1.2.1 YEAST PRIONS

Recently, a novel mode of inheritance has been discovered in *Saccharomyces cerevisiae* (Wickner, 1994; Lindquist, 1997). Phenotypes transmitted by two dominant, cytoplasmically inherited genetic elements, [*PSI+*] and [*URE3*], seem to depend upon the inheritance of altered protein structures, rather than altered nucleic acids. The "protein-only" hypothesis for their inheritance led these elements to be called "yeast prions" (Wickner, 1994). The term "prion" was first coined to describe the infectious agent hypothesized to cause mammalian spongiform encephalogathies (TSEs) by a "protein only" mechanism: a normal cellular protein (PrP^C) adopts an altered conformation (PrP^{Sc}) and interacts with other PrP^C proteins to change their conformation as well (Prusiner, 1996).

The yeast [*PSI+*] element, the subject of the inventor's work, does not generally kill cells. It reduces the fidelity of ribosome translation termination and thereby suppresses nonsense codons (Lindquist, 1997). This phenotype is thought to result from a change in the state of the

translation-termination factor, Sup35, that interferes with its normal function. In [*psi-*] cells, Sup35 is protease sensitive and is mostly soluble; in [*PSI+*] cells, Sup35 has increased protease resistance and is mostly aggregated (Paushkin *et al.*, 1996; Patino *et al.*, 1996; Paushkin *et al.*, 1997). "Aggregate" is used in a general sense; Sup35 may be polymerized into an amyloid-like

5   structure, or coalesced in a less ordered state. When pre-existing Sup35 is in the aggregated state, newly made Sup35 aggregates too, causing a self-perpetuating loss of function in the termination factor and a heritable change in translational fidelity (Patino *et al.*, 1996; Paushkin *et al.*, 1997).

10   [*PSI+*] depends upon the chaperone protein Hsp104. The first known function of Hsp104 was in thermotolerance in yeast, where it increases survival after exposure to extreme temperatures up to 1000-fold (Sanchez and Lindquist, 1990). It does so by promoting the reactivation of proteins that have been damaged by heat and have begun to aggregate (Parsell *et al.*, 1994). At normal temperatures, Hsp104 overexpression cures cells of [*PSI+*]. Sup35

15   becomes soluble and the fidelity of translation termination is restored. This state is heritable, even when overexpression of Hsp104 ceases (Chernoff *et al.*, 1995). Because the only known function of Hsp104 is to alter the conformational state of other proteins, these observations provide a strong argument that [*PSI+*] is indeed based upon a heritable (self-perpetuating) change in the conformational state of Sup35.

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Surprisingly, deletions of *HSP104* also cure cells of [*PSI+*], and Sup35 is soluble in such cells as well (Patino *et al.*, 1996; Chernoff *et al.*, 1995). This is very different from heat-induced aggregates, which remain insoluble in *hsp104* deletion strains. Clearly, the relationship between Hsp104 and [*PSI+*] is more complex than the relationship between Hsp104 and thermotolerance.

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1.2.2   HUMAN PRIONS

The family of transmissible spongiform encephalopathies (TSEs) include scrapie in sheep, bovine spongiform encephalopathy (BSE) or "mad cow disease" in cattle, and several rare human neuropathies: Creutzfeld-Jacob disease (CJD), fatal familial insomnia (FFI), Gertsmann-

30   Straussler-Scheinker (GSS) syndrome, and kuru (Caughey and Chesebro, 1997; Prusiner, 1996).

A central event in TSE pathogenesis is the accumulation in the nervous system of an abnormally-folded version (PrP^{Sc}) of a normal cellular protein, PrP^C. Griffith first proposed a "protein-only" model to explain the unconventional behavior of the infectious TSE agent (Griffith, 1967). Indeed, the "prion", a term by which the agent is popularly known today, appears to be almost entirely proteinaceous: consisting primarily of PrP^{Sc} (Caughey and Chesebro, 1997; Prusiner, 1996).

Several lines of evidence show that PrP^C is conformationally distinct from PrP^{Sc}, although both molecules derive from the same primary sequence and have no detectable post-translational differences (Caughey and Chesebro, 1997; Prusiner, 1996; Caughey *et al.*, 1991; Pan *et al.*, 1993; Riek *et al.*, 1996). The conversion of PrP^C to PrP^{Sc} appears to involve direct interactions of PrP^C with pre-existing PrP^{Sc} (Caughey and Chesebro, 1997; Prusiner, 1996; Kocisko *et al.*, 1994). However, the exact mechanism underlying conversion is not known. Genetic and inhibitor studies have suggested that other cellular factors may influence TSE pathogenesis or serve as regulators of disease (Kenward *et al.*, 1996; Talzelt *et al.*, 1996; Carlson *et al.*, 1988; Caughey *et al.*, 1994; Telling *et al.*, 1995; Edenhofer *et al.*, 1996). None have been conclusively identified; however, cellular osmolytes (sometimes called chemical chaperones; Caughey and Raymond, 1991) and protein chaperones have been frequently speculated to be among them (Kenward *et al.*, 1996; Caughey *et al.*, 1994; Telling *et al.*, 1995; Edenhofer *et al.*, 1996).

2.0 SUMMARY OF THE INVENTION

The chaperone protein Hsp104 controls the genetic behavior of a mysterious yeast prion-like element known as [PSI+]. The chaperone Hsp104 controls the aggregation of Sup35, the protein determinant of [PSI+].

The present invention includes, but is not limited to, the following features:

1) The protein Sup35 forms amyloid-like protein fibers *in vitro*. This is a property shared by other amyloidogenic proteins that cause human disease.

2)   The yeast protein Hsp104 affects the behavior of Sup35 *in vitro*. It also affects the behavior of PrP (the mammalian prion protein) *in vitro* in a similar manner and interacts in a specific manner with β-amyloid peptide 1-42 (Alzheimer's disease peptide).

5   3)   When mammalian PrP is expressed in yeast cells, its folding state depends upon the Hsp104 protein. This is the final element that establishes that yeast can provide an excellent model system for studying factors that affect the folding properties of human disease proteins that have an amyloidogenic character.

10   In important embodiments of the present invention, this yeast system is used in methods of identifying a candidate substance that inhibits the aggregation of an aggregate-prone amyloid protein. Such methods comprise contacting a yeast cell that expresses an aggregate-prone amyloid protein with the candidate substance under conditions effective to allow aggregated amyloid formation, and determining the ability of the candidate substance to inhibit the aggregation of the aggregate-prone amyloid protein.

The term "aggregate-prone amyloid protein" is meant to be any protein that is able to form an amyloid or amyloid-like deposit. Amyloid or amyloid like deposits are generally insoluble fibrillary material. Although many proteins are capable of aggregating at high concentrations, aggregate prone amyloid proteins are able to, and often do, aggregate under physiological conditions, such as inside of a cell. Aggregate-prone amyloid proteins include yeast proteins, such as Sup35 and URE3, and mammalian proteins, such as PrP and β-amyloid polypeptide. The inventors contemplate that a protein of essentially any origin may be used in the present invention.

25   In some preferred embodiments, the aggregate-prone amyloid protein is a chimeric protein. By "chimeric protein" it is meant that the protein comprises polypeptides that do not naturally occur together in a single protein unit. Preferred chimeric proteins comprises at least the N-terminal domain of Sup35. This domain has been found to form aggregates in yeast and *in vitro* and is capable of causing the aggregation of chimeric proteins comprising this domain. 30   Other preferred chimeric proteins include comprises at least an aggregate forming domain of a

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mammalian amyloid polypeptide, such as at least amino acids 1-42 of the β-amyloid protein or at least the aggregate forming domain of PrP. In an important embodiment, the chimeric protein comprises Sup35 in which the N-terminal domain has been replaced by amino acids 1-42 of β-amyloid protein.

In other embodiments, the chimeric protein comprises at least an aggregate forming domain of an aggregate-prone amyloid protein operably attached to a detectable marker protein. By "operably attached" it is meant that the aggregate forming domain and the marker protein are attached such that the chimeric protein maintains the ability to aggregate and the marker protein maintains the property of allowing detection of aggregation of the chimeric protein. For example, the Sup35 N-terminal domain is operably linked to the green fluorescent protein when this polypeptide is capable of aggregating and the aggregated protein maintains the ability of green fluorescent protein to fluoresce.

In other embodiments, the aggregation of the chimeric protein leads to loss of function of the marker protein. When the marker protein is an enzyme, aggregation of the marker protein leads to loss of the enzymatic activity of the marker protein. That is to say that the enzymatic marker protein maintains its enzymatic activity when not aggregated, but aggregation leads to the loss of enzymatic activity. Loss of activity may be due to an alteration of the structure of the marker protein or may be due to sequestering of the protein in the aggregates away form the substrate or cofactors. The enzyme may be luciferase, confer drug resistance, or, in preferred embodiments, have the translation termination activity of the Sup35 protein. In other embodiments, the marker protein is a hormone receptor, such as the glucocorticoid receptor.

The inventors contemplate that the aggregation of the aggregate-prone amyloid protein may be detected in a number of ways. Including the methods described above, the aggregate may be detected by staining with Congo Red. In other embodiments, the aggregation is detected by the characteristic protease resistance of the aggregated protein. The ability to detect the protein may be increased by labeling the aggregate-prone amyloid protein. Labels useful in the detection of the aggregate-prone amyloid protein include radioactive isotope labels, such as ^{35}S,

fluorophores, such as green fluorescent protein, or chromophores. In some preferred embodiments, aggregation is determined by the presence of a [PSI+] phenotype.

Although overexpression of the chimeric protein comprising the aggregate-prone domain of an aggregate-prone amyloid protein often leads to aggregation of the chimeric protein, the inventor has found that this aggregation is dependent on expression of heat shock proteins, such as Hsp104. Therefore, conditions effective to allow amyloid formation may involve modulating the expression of Hsp104 in the yeast cell. In preferred embodiments, the yeast cell overexpresses Hsp104.

In other embodiments of the present invention, the yeast systems are used to identify candidate substances for therapeutic activity against an amyloidogenic disease in an animal. These methods comprise contacting a yeast cell that expresses an aggregate-prone amyloid protein with said candidate substance under conditions effective to allow amyloid formation and determining the ability of said candidate substance to inhibit aggregation of the aggregate-prone amyloid protein. Thus, the ability to inhibit aggregation is indicative of therapeutic activity.

Amyloidogenic diseases in animals include Alzheimer's disease, scrapie, spongiform encephalopathy in a mammal, kuru, Creutzfeldt-Jakob disease, Gestmann-Strausser-Scheinker disease, or fatal familial insomnia. In preferred embodiments, one would express a protein comprising the aggregate forming domain of the etiological agent of a particular disease in the yeast system to identify therapeutic compounds for that particular disease. Therefore, in determining therapeutic compounds for Alzheimer's disease, one would use a yeast system comprising at least amino acids 1-42 of the β-amyloid protein.

Likewise, in determining therapeutic compounds for scrapie, spongiform encephalopathy in a mammal, kuru, Creutzfeldt-Jakob disease, Gestmann-Strausser-Scheinker disease, or fatal familial insomnia, one would use a yeast system comprising the aggregate-forming domain of PrP. In preferred embodiments, the mammalian encephalopathy is bovine, feline, a mink, deer, elk, a mouse, a hamster, an ape, a monkey, or human.

Although many alternative forms of the PrP gene exist, the inventor contemplates that the expression in the yeast of a gene encoding the form linked to a specific disease is preferred for finding therapeutic agents for that disease. For example, for finding therapeutic agents for scrapie, it is preferred that proteins comprising aggregate forming domain of the goat or sheep

5   PrP protein are expressed in the yeast. Of course, due to similarities between the PrP proteins, and even between the different types amyloid proteins, a therapeutic agent for one amyloidogenic disease may have therapeutic activity for one or more other amyloidogenic diseases.

As used herein "a" or "an" will be understood to mean one or more.

10

3.0   BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of

15   specific embodiments presented herein.

FIG. 1A, FIG. 1B and **FIG. 1C.** Specificity of circular dichroism spectral shifts with Hsp104 and Sup35. Right, predicted (--) and actual (–) spectra of mixed proteins. Left, individual spectra used to generate predicted spectra. (A) Sup35 in LSB1 (low salt buffer) with

20   aldolase or Hsp70. (B) Hsp104 and aldolase or IgM in LSB1. (C) Top, Hsp104 and Sup35 in LSB1. Bottom, Hsp104 and Sup35 in HSB (high salt buffer). Data, buffer spectra subtracted, are presented in millidegrees because the possibility of proteins partitioning out of solution invalidates molar ellipticity calculations. Hsp104, Hsp70, aldolase, or the buffer in which they were prepared was directly added to Sup35 at a ~1:2.5 gram-weight ratio. Reactions were

25   incubated for 1 hr with 1 mM ATP at 37°C and spectra were then recorded at 25°C.

FIG. 2A, FIG. 2B, FIG. 2C and **FIG. 2D.** Specificity of circular dichroism spectral shifts with Hsp104 and rPrP. Predicted (--), actual (–) and individual spectra as in FIG. 1. rPrP was prepared and folded into either ß sheet or α helical forms. (A) Hsp104 and rPrPß; (B)

30   GroEL and rPrPß; (C) Aldolase and rPrPß; (D) Hsp104 and rPrPα. Proteins and rPrP were

mixed (each at 0.5 mg/ml) with each other in LSB2. Reactions were incubated at 37°C for 1 hr, diluted 5-fold with cold water, and spectra were measured at 12°C.

FIG. 3A and **FIG. 3B**. Effects of mixing PrP peptides with Hsp104. (A) Location of peptides used in this study. Peptides prepared as in (Zhang *et al.*, 1995) were derived from the hamster PrP sequence except for peptide K, derived from mouse PrP. (B) Effects of PrP peptides on the ATPase activity of Hsp104. Bars extend from the value obtained for Hsp104 without added peptide.

FIG. 4A, FIG. 4B, FIG. 4C and **FIG. 4D**. Specificity of circular dichroism spectral shifts with different PrP peptides. Predicted (--), actual (–) and individual spectra as in FIG. 1. Reactions were performed as in FIG. 2 except that the buffer used was 20 mM Tris, 10 mM $MgSO_4$, 50 mM KCl, 1.25 mM ATP at pH 7.5 to approximate ATPase assay conditions.

FIG. 5A, FIG. 5B, FIG. 5C, FIG. 5D, FIG. 5E and **FIG. 5F**. Effects of chaperones on cell-free conversion of ^{35}S-PrP^C to its protease-resistant form.

FIG. 5A. Conversions (as percent of total ^{35}S-PrP^C) obtained after 24 hours either with PrP^{Sc} or without PrP^{Sc} (100 ng), but with the indicated chaperones (each at 5 μM, with 5 mM ATP), using the standard assay described in methods. In indicated reaction (second from left), PrP^{Sc} was partially-denatured with guanidinium hydrochloride (GdnHCl). Identical results were obtained, over a broad range of chaperone concentrations, with or without ATP.

FIG. 5B. Conversions performed as in A, with the addition of untreated PrP^{Sc}. Mean values are from 3-6 studies, with standard errors. Buffers for storing various chaperones differed slightly in salt and glycerol content, but none affected conversion.

FIG. 5C. Concentration-dependent effects of chaperones in promoting conversion with untreated PrP^{Sc}. Other Hsps tested as in FIG. 5A.

FIG. 5D. SDS-PAGE phosphorimage of ^{35}S-PrP^C products from representative conversion reactions obtained with 3 ng ^{35}S-PrP^C and increasing amounts of PrP^{Sc} (3-1000 ng). One tenth of each reaction was left untreated (-PK); the remainder was digested with proteinase K (+PK). GroEL and GroES were at 1 µM. When indicated, PrP^{Sc} was partially-denatured with GdnHCl. PrP^{Sc} fold represents the ratio of PrP^{Sc}:^{35}S-PrP^C in the reaction.

FIG. 5E. ATP dependence of GroEL-mediated conversions. SDS-PAGE phosphorimages of representative conversion reactions obtained with untreated PrP^{Sc} and GroEL (WT and mutant D87K), with or without ATP. Both proteinase K-treated (+PK; *bottom*) and untreated samples (-PK, one-fifth sample; *top*) are shown.

FIG. 5F. ^{35}S-PrP^{GPI-} conversions with or without chaperones. Reactions contained either untreated PrP^{Sc} or GdnHCl-treated PrP^{Sc}, and a variant PrP missing the GPI anchor, ^{35}S-PrP^{GPI-}. ^{35}S-PrP^{GPI-} and ^{35}S-PrP^C preparations are compared (right panel): UG unglycosylated, MG monoglycosylated, and DG diglycosylated PrP species as indicated.

FIG. 6A, FIG. 6B and **FIG. 6C.** Time course of conversion with or without chaperone.

FIG. 6A. Appearance of PrP-res at 2, 6, 24, and 48 hours, in reactions treated with proteinase K, analyzed by quantitative phosphorimaging of SDS-PAGE. Mean values from three independent measurements, with standard errors.

FIG. 6B. Pelletable ^{35}S-PrP determined by quantitative phosphorimaging of SDS-PAGE. At the indicated times, ^{35}S-PrP reaction products were centrifuged at 15,000Xg for 30 minutes at 22°C. After separating the supernatant fraction (S), the pelletable fraction (P) was resuspended in conversion buffer, and both fractions were prepared for SDS-PAGE. Mean values from three independent studies, with standard errors.

FIG. 6C. Protease-resistant ^{35}S-PrP in pellet (P) and supernatant (S) fractions quantified from SDS-PAGE phosphorimages of 24 hour reactions. Average of two independent studies.

FIG. 7A, FIG. 7B, FIG. 7C and **FIG. 7D**. Combined effects of chaperones and partially-denatured PrP^{Sc} on conversion.

FIG. 7A. Conversions obtained with partially-denatured PrP^{Sc} (4M urea pre-treatment) with buffer alone, or with the indicated chaperones and control proteins (each at 5 μM). Mean values from 3-6 independent measurements, with standard errors.

FIG. 7B. SDS-PAGE phosphorimage of representative conversion reactions obtained with untreated PrP^{Sc} (0) or PrP^{Sc} partially denatured in the presence of increasing urea concentrations (1-5 M), with or without chaperone (Hsp104 or GroEL, 3 μM). Only proteinase K-treated (+PK) samples are shown.

FIG. 7C. SDS-PAGE phosphorimage of representative conversion reactions obtained with Hsp104 (WT or mutant KT218), with or without ATP, and untreated or partially-denatured PrP^{Sc} (4M urea pre-treatment). Only proteinase K-treated samples (+PK) are shown.

FIG. 7D. SDS-PAGE phosphorimage of representative conversion reactions obtained with partially-denatured PrP^{Sc} (4M urea pre-treatment), with or without ATP, and with or without GroEL (WT or mutant D87K). Both proteinase K-treated (+PK; *bottom*) and untreated samples (-PK, one-fifth sample; *top*) are shown.

FIG. 8. Conversion of ^{35}S-PrP^{C} in the presence of chemical chaperones. SDS-PAGE phosphorimages of representative conversion reactions obtained with partially-denatured PrP^{Sc} (4M urea pre-treatment) in the presence of increasing concentrations of DMSO, glycerol, sucrose, or trehalose.

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4.0   DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The invention demonstrates that yeast cells provide a system in which the folding of amyloidogenic proteins from diverse organisms is subject to manipulation. The most immediate application is the use of yeast cells to screen for reagents that affect amyloid formation, a process that is integral to several devastating human diseases. Screening for agents that affect these disease factors is very expensive and time consuming in animal models and cultured cells. Yeast will provide a rapid first screening system to quickly and cheaply identify reagents that affect the folding and aggregation properties of the target protein. These can then be screened by conventional methods to determine which are therapeutically applicable.

The inventor has found that Hsp104 controls the behavior of a factor that alters a particular physiological property of yeast cells in a heritable way. This change in physiology was shown to be associated with a heritable change in the aggregation state of a particular protein, Sup35, that is controlled by genetic manipulation of Hsp104. Subsequently, the inventor demonstrated that Sup35 has a very unusual biochemical property that it shares with certain human disease proteins. Specifically it forms amyloid fibers that stain with the dye Congo Red and shows apple green birefringence. Staining with this dye is a common diagnosis for human amyloid diseases (Glover *et al.*, 1997; incorporated herein by reference).

The present invention is based, in part, on the inventor's discovery that, in a purified system *in vitro*, Hsp104 affects the folding state of the yeast amyloidogenic protein Sup35. Moreover, it also affects the folding state of a mammalian amyloidogenic protein, the prion protein known as PrP. The yeast protein was also shown to interact in a highly specific manner with another mammalian amyloid protein, β-amyloid peptide 1-42 (Alzheimer's disease peptide). The inventor has established that the folding state of the mammalian PrP protein, when expressed in yeast, depends upon the same type of manipulations that the folding of the yeast amyloid Sup35 depends upon. This establishes that yeast provides a surprisingly advantageous and widely applicable system for testing factors that affect the folding and amyloidogenic properties of mammalian disease proteins (Schirmer and Lindquist, 1997; DebBurman *et al.*, 1997).

4.1 Methods of Screening and Selecting Amyloid Formation

The inventor contemplates that the formation of amyloid fibers may be detected by a number of mechanisms. In some embodiments, the aggregation may be detected by its ability to bind Congo Red and show apple green birefringence under polarized light (Baker *et al.*, 1994; Guiroy *et al.*, 1993; Gasset *et al.*, 1992; Tashima *et al.*, 1986; Bockman *et al.*, 1985; Bendheim *et al.*, 1984; Prusiner *et al.*, 1983). However, in other embodiments, the aggregation is detected indirectly. For example, in embodiments comprising the Sup35 aggregation domain (N-terminal domain), the physiologically important C-terminal domain may be sequestered in the cell by the addition of the endogenous Sup35 protein into the aggregation, causing a change in phenotype of the cell. Thus, aggregation may be detected by the presence of the [PSI+] phenotype in the yeast cells. Depending upon how much of the Sup35 comprising protein is expressed and aggregated in the yeast, this phenotype is characterized by an increase in nonsense suppression, lesser aggregation, or cell death, higher aggregation.

Chernoff *et al.* (1995) used a color test for the [PSI+] phenotype. In this test, a *ade1-14* strain was used. In this strain, the *ade1-14* nonsense mutation is suppressed in the presence of the [PSI+] phenotype. This leads to white colored colonies. In the absence of the [PSI+] phenotype, this strain has a red color. This test provides a screen for the [PSI+] phenotype. Therefore, the ability of conditions or compositions to affect the [PSI+] phenotype may be detected by their ability to affect a color change in this [PSI+]/*ade1-14* strain.

In some preferred embodiments, the [PSI+] phenotype kills the yeast cell. Such cells are particularly useful in screening for the [PSI+] phenotype. For example, yeast expressing a chimeric protein comprising the β-amyloid peptide (1-42) and the Sup35 C-terminal domain have a [PSI+] phenotype that leads to cell death. The inventor contemplates that such cells are an excellent system for screening candidate compounds for their ability to inhibit β-amyloid aggregation, because only yeast grown in the presence of compounds that inhibit or reverse the [PSI+] phenotype will survive.

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The inventor has shown that chimeric proteins comprising an aggregate prone domain have prion properties. For example, in a yeast expressing a chimeric protein comprising the N-terminal domain of Sup35 and GFP, the GFP was shown to aggregate. This same result was seen in a yeast strain expressing a chimeric protein comprising the N-terminal domain of Sup35 and GFP but that lacked expression of the N-terminal domain of the endogenous Sup35. This shows the aggregation of the chimeric protein was independent of the endogenous protein comprising the aggregate prone domain. Furthermore, chimeric proteins comprising GFP may be particularly useful in methods of screening agents that prevent aggregation, as the fluorescence pattern GFP is quickly and easily screened.

The inventor contemplates that, because chimeric proteins comprising an aggregate prone domain take on prion-like properties in yeast, such proteins are useful in developing screens or selections for the presence of aggregation. When a chimeric protein comprising an aggregate prone domain, such as the N-terminal domain of Sup35, and another polypeptide, such as luciferase or the glucocorticoid receptor, is expressed in yeast under conditions that lead to aggregation, aggregation of the chimeric protein leads to changes in the activities of the other polypeptide. Therefore, in yeast cells comprising the Sup35 aggregate prone domain and luciferase, the presence of aggregation can be detected by the loss of luciferase activity in the cells. In other preferred embodiments, the chimeric protein comprises an aggregate prone domain and a drug-resistance marker. In such embodiments, aggregation leads to antibiotic sensitivity.

4.2   AMYLOID DISEASES

In an important embodiment, the present invention is a screen for compounds that are therapeutic for amyloid diseases. The inventors contemplate that, by using polypeptides comprising the etiological agent of the amyloid disease, the methods of the present invention may be used to find therapeutic compounds for essentially any amyloid disease. A number of amyloid diseases occur in mammals and are discussed herein.

A number of neurodegenerative diseases in mammals have been linked to the aggregation of the product of the PrP gene (prion protein). Such diseases include scrapie in sheep and goats,

mad cow disease (bovine spongiform encephalopathy), transmissible mink encephalopathy, chronic wating disease in captive mule deer and elk, feline spongiform encephalopathy, and prion diseases of other animals including mice, hamsters, nyala, greater kudu, eland, gembok, arabian oryx. Of course, prion diseases are also seen in apes, monkeys, and humans.

In humans, as in many animals, prion diseases can be sporadic, inherited, or may be brought on by inoculation with infectious prion particles. Common names of prion diseases in humans are kuru, Creutzfeld-Jakob disease (CJD), Gerstmann-Straussler-Scheinker (GSS), and fatal familial insomnia (FFI). The classification of human prion diseases is based on clinical and neuropathological findings (Prusiner, 1996; incorporated herein by reference).

Prion diseases resulting from the horizontal transmission of infectious prions are iatrogenic CJD and kuru. Inherited forms GSS, familial CJD, and FFI have all been associated with oneor more mutations in the protein coding region of the PrP gene (Bertoni *et al.*, 1992; Dlouhy *et al.*, 1992; Doh-ura *et al.*, 1989; Gabizon *et al.*, 1993; Goldfarb *et al.*, 1990; Goldfarb *et al.*, 1991; Goldfarb *et al.*, 1992; Goldgaber *et al.*, 1989; Hsiao *et al.*, 1989; Kitamoto *et al.*, 1993a; Kitamoto *et al.*, 1993b; Medori *et al.*, 1992; Petersen *et al.*, 1992; Poulter *et al.*, 1992). Sporadic forms of prion disease in humans comprise most cases of CJD and some cases of GSS (Masters *et al.*, 1978).

Regardless of the origin of the prion diseases, all have been associated with abnormal folding of the cellular protein PrP^c into a protease resistant form, PrP^{sc}, that aggregates (Oesch *et al.*, 1985; Bolton *et al.*, 1982; McKinley *et al.*, 1982; Bolton *et al.*, 1984; Prusiner *et al.*, 1984; Bolton *et al.*, 1987).

Another amyloid disease in humans is Alzheimer's disease (AD). One of the key events in AD is the deposition of amyloid as insoluble fibrous masses (amyloidogenesis) resulting in extracellularneuritic plaques and deposits around the walls of cerebral blood vessels (WO 96/39834; incorporated herein by reference). The main component of amyloid is a 4.1-4.3 kDa peptide, called β-amyloid, that is part of a much longer amyloid precursor protein APP (Muller-

Hill and Beyreuther, 1989). Peptides containing the sequence 1-40 or 1-42 of β-amyloid and shorter derivatives can form amyloid-like fibrils in the absence of other protein (Pike *et al.*, 1993).

The inventors have shown that proteins comprising PrP and β-amyloid polypeptides are capable of forming aggregates in a yeast based system. Thus, this system provides a mechanism of testing compounds for their ability to inhibit the aggregation of these polypeptides in an inducible, yeast-based system. Such compounds may be used as amyloid disease therapeutic compounds.

5.0 EXAMPLES

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

5.1 EXAMPLE 1 -- INTERACTIONS OF THE CHAPERONE HSP104 WITH YEAST SUP35 AND MAMMALIAN PRP

A critical missing link in the "protein-only" hypothesis for [*PSI+*] inheritance is any evidence that Hsp104 actually interacts directly with Sup35. Indeed, little is known about the interaction of Hsp104 with any substrate, as the heat-denatured aggregates that constitute its other likely *in vivo* substrates are inherently difficult to study. Here the inventor provides evidence for a highly specific interaction *in vitro* between Hsp104 and Sup35. This interaction produces a change in protein structure and inhibits the ATPase activity of Hsp104. The inventor also reports that Hsp104 interacts in a remarkably similar way with mammalian PrP, the protein determinant of the neurodegenerative "prion" diseases (Prusiner, 1996; Caughey and Chesebro, 1997), and with ß-amyloid peptide (Glenner and Wong, 1984).

5.1.1 MATERIALS AND METHODS

5.1.1.1 PROTEIN AND PEPTIDE PREPARATION

Hsp104 (prepared as in 12), Hsp70 (obtained from J. Glover), aldolase (Pharmacia), and IgM (Rockland) were stored in 20 mM Tris pH 8.0, 2 mM EDTA, 1.4 mM ß-mercaptoethanol, 5% glycerol, 1 mM 4-(2-aminoethyl)benzenesulfonyl fluoride (AEBSF). Sup35 and the fragment MN (purified as in 13) were dialyzed against HSB (high salt buffer, 20 mM HEPES pH 7.5, 10 mM $MgCl_2$, 140 mM KCl, 15 mM NaCl freshly supplemented with 5 mM ß-mercaptoethanol and 1 mM AEBSF) to remove imidazole, and then dialyzed against either HSB or LSB (low salt buffer, 10 mM MES pH 6.5, 10 mM $MgSO_4$). Concentrations were determined by the Bradford assay with BSA (bovine serum albumin) as a standard. Concentrations of PrP (prepared and folded into either ß sheet or α helical forms; Mehlhorn *et al.*, 1996; Zhang *et al.*, 1997), PrP peptides (as in 16), and ß-amyloid (Sigma) were determined spectroscopically using calculated extinction coefficients.

5.1.1.2 ATPASE ASSAYS

PrP peptides (1 mM resuspended in H_2O were assayed in 40 mM Tris pH 7.5, 175 mM NaCl, 5 mM $MgCl_2$, and 5 mM ATP in a 25 µl reaction volume containing 1 µg of Hsp104. Peptides A, G, H, and K were resuspended in dimethyl sulfoxide (DMSO) which was also added to controls containing Hsp104 alone. Effects of other proteins on Hsp104's ATPase activity were measured in LSB or HSB. Phosphate released (mean and standard deviation of at least 3 independent reactions) after 8 minutes at 37°C was measured with Malachite Green (Lanzetta *et al.*, 1979).

5.1.1.3 SPECTROPOLARIMETRY

Hsp104, Hsp70, aldolase, IgM or storage buffer were added to Sup35 or rPrP in the buffers indicated. When aldolase and IgM were tested as substrates of Hsp104, they were first dialyzed against HSB and subsequently LSB, so that their treatment matched that of Sup35. In LSB Sup35 solutions were somewhat cloudy, suggesting some aggregation, but little or no protein precipitated to the bottom of cuvettes during analysis. Chaperones and control proteins were added to Sup35 at a ~1:2.5 gram-weight ratio (*e.g.* Sup35 at ~ 0.4 mg/ml and Hsp104 at

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0.15 mg/ml). Reactions were incubated for 1 hr with 1 mM ATP at 37°C, and transferred to a 0.1 mm path-length cuvette. Spectra were recorded at 25°C in a Jasco 715 spectropolarimeter (bandwidth 1.0 nm, response time 16 sec, speed 20 nm/min, step resolution 0.2 nm, accumulations 4).

Proteins and rPrP were mixed with each other (each at 0.5 mg/ml) or with the appropriate storage buffer in LSB2: 20 mM phosphate buffer pH 6.5, 10 mM MgSO4, 1.25 mM ATP. PrP peptides were mixed with Hsp104 in 20 mM Tris buffer containing 10 mM MgSO4, 50 mM KCl, and 1.25 mM ATP at pH 7.5 to approximate ATPase assay conditions. After 1 hr at 37°C, reactions were diluted 5-fold with cold water, and spectra were measured at 12°C as above. (A larger spectral shift was observed with these conditions for peptide F, presumably because the structural changes obtained with this peptide are unstable at higher temperatures. Although temperature had little effect on the spectra obtained with other peptides or rPrP, for consistency, 12°C was used for all.).

5.1.1.4 CONGO RED DYE BINDING ASSAYS

Reaction conditions were as for CD studies with the addition of Congo red to a final concentration of 10 μM. After 30 min at 25°C, absorbances at 320, 477, and 540 nm were determined. Congo red dye binding was measured using the equation $[(OD_{540}/25,295) - (OD_{477}/46,306)]$ (Klunk et al., 1989).

5.1.2 RESULTS

5.1.2.1 CIRCULAR DICHROISM OF HSP104 AND SUP35 MIXTURES

Attempts to detect an interaction between Sup35 and Hsp104 by co-immunoprecipitation or by affinity chromatography with immobilized Hsp104 were unsuccessful suggesting that if Hsp104 interacts with Sup35, this interaction is weak, transient, or depends upon unique conditions, conformations, or cofactors. Since changes in the expression of Hsp104 lead to changes in the physical state of Sup35 in vivo, as an alternative mechanism for probing interactions between these proteins, the inventor discovered that changes in state could be detected by circular dichroism when purified Hsp104 and Sup35 were mixed in vitro. If two

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proteins do not interact, or if they interact without a substantial change in secondary structure, the CD spectrum of their mixture should equal that predicted from the simple addition of their individual spectra.

5   When either Sup35 or Hsp104 was mixed with any of several control proteins – aldolase, immunoglobulins (IgG and IgM), α-2 macroglobulin, apoferritin, and α-lactalbumin – observed spectra matched the predicted spectra (FIG. 1A and FIG. 1B). These control proteins encompass a wide variety of structural features, including proteins that are largely α-helical or ß-sheet, monomeric or oligomeric, large or small. Furthermore, spectral shifts observed when another

10   chaperone, Hsp70, was mixed with Sup35 were small (FIG. 1A).

         In contrast, when Hsp104 and Sup35 were mixed, the observed spectrum differed dramatically from the predicted spectrum (FIG. 1C, top right). Thus, these two proteins interacted in a highly specific manner to produce a change in the physical state of one or both

15   proteins. ATP is required for some Hsp104 functions (Parsell *et al.*, 1994; Schirmer *et al.*, 1996), but was not required for the change in CD spectrum with Sup35 and Hsp104. However, ATP markedly increased the rate at which this change occurred (Table 1).

TABLE 1
ATP affects rate of CD change

Time, min	-ATP	+ATP
0	2.9	2.2
3	7.9	15.2
6	9.9	17.2
10	10.9	18.2
15	11.8	18.8
20	12.4	19.2
30	13.3	19.8
72	16.2	21.9

20

The difference between the actual spectrum and the predicted spectrum at 225 nm for each timepoint is presented in millidegrees. In each of three separate studies, the spectral change in mixtures of Sup35 and Hsp104 proceeded more rapidly with ATP than without ATP, although the absolute rates varied, most likely due to differences in the Sup35 preparations.

The interaction between Hsp104 and Sup35 apparently depended upon the structural state of Sup35. When Sup35 was dialyzed against low salt buffer at pH 6.5 (LSB, FIG. 1C, top left, solid line) or a higher salt buffer at pH 7.5 (HSB, FIG. 1C, bottom left, solid line) a difference in the CD spectra indicated that the protein was in a different structural state. When Hsp104 was added, the actual CD spectrum deviated from the predicted spectrum only when Sup35 had been dialyzed in LSB (FIG. 1C, compare right panels). Mixtures of Sup35 and several control proteins showed no deviation from predicted spectra in LSB or HSB. Similarly, control proteins mixed with Hsp104 showed no spectral shifts in either buffer. Moreover, the CD spectrum of Hsp104 itself did not change with the buffer (FIG. 1C, left panels, dashed line).

5.1.2.2 SUP35 AGGREGATION

In vivo, the inheritance of [*PSI*+] is associated with the partitioning of Sup35 into aggregates, a change in state that requires Hsp104 (Paushkin *et al.*, 1996; Patino *et al.*, 1996; Chernoff *et al.*, 1995). *In vitro*, Sup35 forms highly ordered, amyloid-like fibers after prolonged incubations in the absence of Hsp104 (Glover *et al.*, 1997). In CD studies the proteins did not precipitate to the bottom of the cuvette or exhibit significant binding to the walls of the tube. However, the upward shift in the spectrum might be due, at least in part, to a partitioning of protein from solution while it remains in suspension (We and Chen, 1989).

To determine whether the interaction between Hsp104 and Sup35 detected by CD analysis *in vitro* is related to the biological interaction between the two proteins *in vivo*, the inventor investigated their association and changes in protein aggregation. Solutions containing mixtures of Sup35 and Hsp104 invariably scattered more light at 320 nm (typically ~30% more) than the simple sum of light scattering by each protein alone. An increase in Congo red dye binding was also detected by the characteristic spectral shift that occurs when this dye binds amyloid proteins (Klunk *et al.*, 1989).

5.1.2.3 EFFECTS OF SUP35 ON THE ATPASE ACTIVITY OF HSP104

When other members of the HSP100 (clp) family are incubated with substrates, the rate at which they hydrolyze ATP is increased (Maurizi *et al.*, 1994; Hwang *et al.*, 1988; Wawrzynow *et al.*, 1995). Thus, changes in the ATPase activity of Hsp104 provide another method for detecting an interaction with Sup35. When assayed in HSB, in which no CD changes were observed, Sup35 weakly stimulated the ATPase activity of Hsp104 (Table 2). Surprisingly, in LSB, in which CD changes were observed, Sup35 strongly inhibited the ATPase activity of Hsp104.

TABLE 2

Effects of proteins and peptides on the ATPase activity of Hsp104

	HSB	LSB
Hsp104 alone	1.0 +/- 0.05	1.0 +/- 0.1
Sup35	1.2 +/- 0.1	0.6 +/- 0.1
N-term Sup35	1.2 +/- 0.1	0.7 +/- 0.1
PrPß	1.2 +/- 0.1	0.6 +/- 0.05
ß-amyloid 1-42	0.8 +/- 0.05	0.3 +/- 0.05
ß-amyloid 1-40	1.1 +/- 0.05	0.5 +/- 0.1
reverse amyloid 40-1	1.1 +/- 0.1	0.8 +/- 0.1
aldolase	1.1 +/- 0.05	1.0 +/- 0.1
BSA	1.0 +/- 0.05	1.0 +/- 0.05
apoferritin	1.0 +/- 0.1	1.0 +/- 0.05
IgM	1.1 +/- 0.05	1.1 +/- 0.05

Hsp104 ATPase activity was measured in HSB or LSB1 and is presented as the activity of Hsp104 with protein divided by the activity of Hsp104 in buffer alone. Within individual studies very little variance was observed; however, even with the results from three different preparations of Sup35 averaged here, only ~10% variability was observed.

Previous studies identified the N-terminal domain of Sup35 as the essential "prion-determining" region (Ter-Avanesyan *et al.*, 1993). This domain is also responsible for the formation of self-seeded amyloid fibrils by Sup35 *in vitro*. (Glover *et al.*, 1997; King *et al.*, 1997). The ATPase activity of Hsp104 was inhibited by this domain to an extent similar to that observed with Sup35 itself (Table 2).

5.1.2.4 EFFECTS OF OTHER AMYLOIDS ON THE ATPASE ACTIVITY OF HSP104

The expansion of the mammalian prion hypothesis to the yeast [*PSI*+] element was initially based upon genetic arguments. PrP and Sup35 are unrelated in sequence and in biological function (Wickner, 1994; Lindquist, 1997; Chernoff *et al.*, 1995). Nonetheless, the capacity for both proteins to form amyloid-like aggregates (Glover *et al.*, 1997; Prusiner *et al.*, 1983; Gasset *et al.*, 1992) suggests an underlying biochemical similarity between them. The inventor investigated whether this similarity would extend to shared molecular features in the two proteins that allow recognition by Hsp104.

The change in state of mammalian PrP associated with TSEs is characterized by increased ß-sheet content and protease resistance in amino-acid segment 90 to 231 (Prusiner *et al.*, 1982; Caughey *et al.* 1991). A recombinant hamster protein corresponding to this segment, in a ß sheet-rich conformation, rPrPß (Mehlhorn *et al.*, 1996; Zhang *et al.*, 1997), produced the same unexpected effect on the ATPase activity of Hsp104 as did Sup35 (Table 2).

The inventor also tested another amyloidogenic peptide, ß-amyloid 1-42, a fragment often found in the neural plaques associated with Alzheimer's disease (Glenner and Wong, 1984). Again, the ATPase activity of Hsp104 was inhibited (Table 2). Less inhibition was observed with a less amyloidogenic derivative, ß-amyloid 1-40, still less with a peptide containing the same amino acids in the reverse order, and no inhibition was observed with a wide variety of control proteins (Table 2). Thus, the unexpected inhibitory effects of these three amyloidogenic polypeptides on Hsp104's ATPase activity are specific and strongly suggest an underlying biochemical similarity between them.

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5.1.2.5 Circular Dichroism of Hsp104 and PrP Mixtures

When Hsp104 was mixed with rPrPß (Mehlhorn *et al.*, 1996; Zhang *et al.*, 1997), the CD spectrum of the solution differed dramatically from the spectrum predicted by the addition of individual spectra (FIG. 2A, right). This result was very reproducible in both degree and effect, with two different preparations of rPrP and two of Hsp104. When rPrPß was mixed with several other chaperones, only GroEL (Hsp60) yielded a substantial spectral shift (FIG. 2B right). Other chaperones (Cdc37, Hsp90, Hsp70), as well as some non-chaperone proteins (apoferritin, ß-galactosidase, α2-macroglobulin, and α-lactalbumin) yielded spectral shifts with PrP, but they were much smaller than those observed with Hsp104 and GroEL. Finally, when rPrPß was mixed with BSA or aldolase (FIG. 2C right), predicted and actual spectra were virtually identical.

As with Sup35, the interaction between Hsp104 and rPrP depended upon the structural state of rPrP. When rPrP was pre-incubated under conditions (Mehlhorn *et al.* 1996; Zhang *et al.*, 1997) that promote an α-helical conformation (rPrPα) rather than a ß sheet-rich conformation (rPrPß), and mixed with Hsp104, the actual spectrum matched the predicted spectrum (FIG. 2D, right). The α-helical and ß sheet-rich forms of rPrP, once acquired, were stable after transfer to the same buffer. Since they were in the same buffer when mixed with Hsp104, the different results obtained with rPrPα and rPrPß can be attributed to an effect of substrate structure on interaction with Hsp104, rather than to an effect of buffer.

5.1.2.6 Correlation Between Structural Transitions and ATPase Inhibition With PrP Peptides

Since for both Sup35 and PrP, the inhibition of Hsp104's ATPase activity occurred under the same conditions where a spectral shift occurred, the inventor postulated that these amyloidogenic proteins might inhibit the ATPase activity of Hsp104 by coupling it to a major change in structure. To investigate this possibility further, the inventor took advantage of various PrP peptide derivatives (FIG. 3A) and the structural transitions of both PrP and these derivatives (Mehlhorn *et al.* 1996; Zhang *et al.*, 1997; Zhang *et al.*, 1995; Gasset *et al.*, 1992; Nguyen *et al.*, 1995). Several peptides from the amino-terminal region had little or no effect on

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the ATPase activity of Hsp104 (FIG. 3B, peptides A and B); a peptide corresponding to amino acids 90-145 strongly stimulated ATP hydrolysis by Hsp104 (FIG. 3B, peptide F); several peptides derived from the carboxy-terminus inhibited it (FIG. 3B, peptides G to K).

5   Peptides with different effects on the ATPase activity of Hsp104 were then tested for spectral shifts in the presence of Hsp104. When peptide B was mixed with Hsp104, the CD spectrum was equivalent to that predicted from the addition of the individual spectra (FIG. 4A). The actual and predicted spectra of Hsp104 and peptide F were not identical, but the deviation was small (FIG. 4B). In contrast, the spectra obtained from mixing Hsp104 with the carboxyl-

10   terminal peptides G and J were very different from the predicted spectra (FIG. 4C and FIG. 4D). Thus, the PrP peptides that inhibited the ATPase activity of Hsp104 yielded the strongest spectral shift.

5.1.3   DISCUSSION

The dependence of [$PSI+$] on the protein chaperone Hsp104 provides one of the strongest genetic arguments that the inheritance of a phenotypic trait can be due to the inheritance of a

15   change in protein conformation, in this case, the conformation of Sup35 (Paushkin et al., 1996; Patino et al., 1996; Chernoff et al., 1995). The validity of this argument rests on two assumptions, 1) that Hsp104 and Sup35 interact directly, and 2) that this interaction influences the

20   physical state of Sup35. Here the inventor provides evidence in support of both. Remarkably, very similar results were obtained with PrP, the mammalian protein whose altered conformation is thought to propagate the transmissible spongiform encephalopathies (Prusiner, 1996; Caughey and Chesebro, 1997). ß-amyloid, the peptide whose deposition in amyloids is thought to contribute to Alzheimer's disease (Glenner and Wong, 1984) also interacted with Hsp104 in a

25   similar manner. These findings reveal an underlying biochemical similarity between these otherwise unrelated proteins.

Circular dichroism studies provided one line of evidence for the direct interaction of Hsp104 with Sup35 and with PrP. The actual spectra observed when Hsp104 is mixed with either

30   of these proteins is different from the spectra predicted by the simple addition of their individual

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spectra. These spectral shifts are highly specific. When control proteins, encompassing a wide variety of structural features, are mixed with Hsp104, actual spectra match the predicted spectra. Further, when Sup35 or rPrPß are mixed with control proteins (including other chaperones) spectral deviations are relatively small, or undetectable (except in the case of rPrPß and GroEL).

5   Finally, the interactions of Hsp104 with Sup35 and PrP themselves appear to depend upon the initial structural states of Sup35 and PrP.

Currently, producing different structural states of Sup35 depends upon using different buffers and, although these buffers did not influence Hsp104's CD spectum, they might influence

10   Hsp104's interaction with Sup35. However, in the case of rPrP distinct conformational states, once established, are stable on transfer to the same buffer (Mehlhorn *et al.* 1996; Zhang *et al.*, 1997). A large spectral shift occurs with rPrPß, a ß sheet-rich, multimeric conformation (Zhang *et al.*, 1997) thought to be associated with TSE diseases, but not with rPrPα, an α helix-rich, monomeric conformation thought to mimic the normal cellular form.

15

The ability of both Sup35 and PrP to inhibit the ATPase activity of Hsp104 provides independent evidence for an interaction between these proteins. The same specificity was observed as with CD: 1) control proteins do not inhibit the ATPase activity of Hsp104, 2) Sup35 inhibits it under the conditions that lead to a change in CD spectrum, but not under the conditions

20   where no change in CD spectrum occurred, and 3) rPrPß also inhibited it under the conditions that lead to a change in the CD spectrum. Studies with a series of peptides spanning the PrP sequence provide another link between the Hsp104::substrate interactions that lead to structural transitions and those that inhibit ATPase activity. The strongest inhibition in Hsp104's ATPase activity occurred with the peptides that produced the strongest CD shifts.

25

The inhibition of Hsp104's ATPase activity was itself surprising. Interactions between other HSP100 proteins and their substrates generally stimulate the chaperone's ATPase activity (Maurizi *et al.*, 1994; Hwang *et al.*, 1988; Wawrzynow *et al.*, 1995). At least some of these interactions, however, seem to involve less dramatic structural transitions (Schirmer *et al.*, 1996).

30   For example, ClpA (an *E. coli* relative of Hsp104) converts the RepA protein from diers to

monomers (Wickner *et al.*, 1994). Both ClpA and Hsp104 are hexameric proteins with multiple ATP binding sites and, presumably, multiple substrate binding sites. Perhaps the structural transitions of more complex, amyloidogenic substrates involve more coupled or "concerted" work from the chaperone and this inhibits its free-running ATPase activity.

5

It is striking that this ß-amyloid peptide also inhibited the ATPase activity of Hsp104. ß-amyloid, Sup35, and PrP differ in size and biological function and have unrelated sequences (except for weak homology in a few oligopeptide repeats of Sup35 and PrP). Yet, all share the capacity to assemble into amyloid-like aggregates (Glenner and Wong, 1984; Glover *et al.*, 1997;

10 Prusiner *et al.*, 1983). The [*PSI+*] genetic trait is linked to the aggregation of Sup35; the pathologies of TSEs and Alzheimer's disease are generally associated with the aggregation of PrP and ß-amyloid respectively (Prusiner, 1996; Caughey and Chesebro, 1997; Glenner and Wong, 1984). Presumably, it is the shared capacity for such conformational transitions that leads to recognition by Hsp104.

15

5.2 EXAMPLE 2 -- CHAPERONE-SUPERVISED CONVERSION OF PRION PROTEIN TO ITS PROTEASE-RESISTANT-FORM

Shown in this example is an assessment of whether or not molecular chaperones, whose known functions are to alter the conformational states of proteins (Hartl, 1996; Buchner, 1996;

20 Parsell and Lindquist, 1993), regulate the conversion of PrP^C to PrP^{Sc}. To test for chaperone involvement, the inventor used a cell-free assay, wherein metabolically-labeled $^{35}S-PrP^C$, purified from cultured cells in an acid-treated state, is converted to a conformational state characteristic of PrP^{Sc} (Kocisko *et al.*, 1994; Caughey *et al.*, 1995). In this altered state, PrP is aggregated and a specific portion of the molecule is highly resistant to proteolysis.

25

This simple *in vitro* conversion reaction faithfully recapitulates several salient TSE features. First, like experimental TSEs, *in vitro* conversion of PrP^C to its protease-resistant form requires pre-existing PrP^{Sc} (Kocisko *et al.*, 1994; Caughey *et al.*, 1995; Bessen *et al.*, 1995; Kocisko *et al.*, 1995). Secondly, strain-specific PrP^{Sc} protease digestion properties, specifically

30 those associated with two mink TSE strains – hyper and drowsy, were precisely propagated from

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PrP^{Sc} to radiolabeled PrP^C in this assay (Bessen *et al.*, 1995). Thirdly, the known *in vivo* barriers to transmitting TSEs between different species were reflected well in the efficiencies of *in vitro* conversion (Kocisko *et al.*, 1995; Raymond *et al.*, 1997). Lastly, this cell-free assay modeled accurately another *in vivo* TSE barrier, based on genetic polymorphisms in PrP, which render

5   sheep either highly susceptible, moderately susceptible, or resistant to scrapie (Bossers *et al.*, 1997).

Together, these studies provide substantial evidence that *in vitro* converted, protease-resistant PrP is either authentic PrP^{Sc} or has a very similar conformation. The *in vitro* converted

10   material is operationally referred to herein as protease-resistant PrP (PrP-res).

Here, the inventor provides the first evidence that molecular chaperones can regulate conformational transitions in PrP. Two protein chaperones, GroEL and Hsp104, promoted *in vitro* conversion, in contrast, the chemical chaperones, sucrose, trehalose, and DMSO inhibited

15   it. Importantly, the inventor's results with chaperones demonstrate that *in vitro* converted PrP-res is a bonafide conformationally-altered PrP molecule. Chaperones provide new understanding of the nature of PrP intermediates involved in PrP conversion, and provide evidence that the conversion process has two steps. The ability of chaperone-like molecules to supervise PrP^{Sc} formation in TSEs *in vivo* means that these molecules represent important clinical targets to

20   combat this dreaded disease.

5.2.1   MATERIALS AND METHODS

5.2.1.1   CHAPERONE PROTEINS

Yeast Hsp40 (Ydj1), Hsp70 (ssa1/ssa2), and Hsp104 (WT and mutant) were

25   purified as previously described (Cyr *et al.*, 1992; Zeigelhoffer *et al.*, 1995; Parsell *et al.*, 1993) and were obtained from J.R. Glover and Y. Kimura. Bacterial GroES and GroEL (WT and mutant) were obtained by A.L. Horwich. Hsp26 was obtained from T. Suzuki and E. Vierling, and Yeast Hsp90 was obtained by J. Buchner.

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5.2.1.2 CHAPERONE FOLDING ASSAYS

Hsp104 promoted the refolding of kinetically-trapped denatured luciferase, but only when Hsp40, Hsp70 and ATP were also present (J.R. Glover and S. Lindquist, manuscript in preparation). The function of other chaperones were assessed using previously published procedures. GroEL and GroES activities were measured by the refolding of denatured rhodanese (Mendosa *et al.*, 1991); Hsp90 suppressed the aggregation of β-galactosidase (Freeman and Morimoto, 1996); Hsp26 activity was measured by the suppression of aggregation of malate dehydrogenase (Lee *et al.*, 1995).

5.1.1.3 PRP PURIFICATION

PrP^{Sc} was purified from hamsters infected with 263K strain of scrapie as previously described (Kocisko *et al.*, 1994). Hamster ^{35}S-PrP^C and ^{35}S-PrP^{-GPI-} proteins were purified from cultured cells by a procedure described in B. Caughey *et al.*, (1996) (Caughey *et al.* 1995), except that radiolabeled proteins were eluted with 0.1M acetic acid at 22°C for 30 minutes and stored at 4°C before use. To obtain non-glycosylated ^{35}S-PrP^C, cultured cells were pre-incubated and ^{35}S-labeled in the presence of 2 µg/ml tunicamycin (Boehringer-Mannheim), an inhibitor of glycosylation (Caughey *et al.*, 1995).

5.2.1.4 CELL-FREE PRP CONVERSION

Unless otherwise stated, all reactions were performed using the same modification of a published procedure (Caughey *et al.*, 1995). ^{35}S-PrP^C (20,000 cpm ~3 ng) denatured in 0.1M acetic acid was diluted into 1X conversion buffer (CB: 50 mM sodium citrate-HCl, pH 6.0, supplemented with 1% N-lauryl sarkosine). PrP^{Sc} (100 ng) was incubated with ^{35}S-PrP^C (20 µl volume) at 37°C for 24 hours. When indicated, PrP^{Sc} was pretreated for one hour with either 2M GdnHCl at 37°C or 4M urea at 22°C; in conversion reactions, GdnHCl and urea were present at 0.2M and 0.4M respectively. In chaperone-mediated conversions, chaperones (1 µM, unless otherwise stated) were added to CB prior to the addition of ^{35}S-PrP^C and PrP^{Sc}. Reactions with chaperones contained 10 mM $MgCl_2$, 1.5 mM NaCl, and 140 mM KCl, and unless otherwise stated, 5 mM ATP. All reactions with ATP included an ATP regenerating system containing 20

mM phosphocreatine and 10 µg/ml creatine phosphokinase. These supplements did not affect PrP conversion.

For each reaction, one-tenth to one-fifth of the sample was left untreated for determination of percent conversion of ^{35}S-PrP^C to PrP-res (Caughey *et al.*, 1995). The remainder was digested with proteinase K (PK; 80 µg/ml) for 1 hour at 37°C, and both PK-untreated and PK-treated samples were prepared for SDS-PAGE (Caughey *et al.*, 1995). ^{35}S-PrP products were visualized in dried gels by phosphorimaging and quantified with ImageQuant software (Molecular Dynamics).

5.2.2 RESULTS

5.2.2.1 CHAPERONES ALONE DO NOT CONVERT PrP^C TO PrP-RES

The inventor first examined the ability of major cellular chaperones GroES (Hsp10), Hsp26, Hsp40, GroEL (Hsp60), Hsp70, Hsp90, and Hsp104, to promote ^{35}S-PrP^C conversion in the absence of PrP^{Sc}. These chaperones were chosen because they employ different mechanisms to affect the conformation and physical state of other proteins (Hartl, 1996; Buchner, 1996; Parsell and Lindquist, 1993). In separate studies, these same chaperone preparations functioned appropriately in a variety of protein folding assays. Yet, over a broad range of concentrations, alone and in various combinations, with (FIG. 5A) or without ATP, none of these chaperones promoted the conversion of PrP^C to PrP-res, in the absence of PrP^{Sc}. This observation strongly underscores the importance of pre-existing PrP^{Sc} in the conversion of PrP^C.

5.2.2.2 GROEL PROMOTES CONVERSION IN REACTIONS NUCLEATED WITH UNTREATED PRP^{Sc}

Next, the inventor determined whether chaperones influenced ^{35}S-PrP^C conversion in the presence of PrP^{Sc}. To date, efficient *in vitro* conversion of PrP^C to PrP-res has usually required partial chemical denaturation of PrP^{Sc} (left bars, FIG. 5A; Edenhofer *et al.*, 1996; Freeman and Morimoto, 1996). Untreated and completely denatured PrP^{Sc} (6M GdnHCl pretreatment) have little (FIG. 5D) and no converting ability respectively (Kocisko *et al.*, 1994; Caughey *et al.*, 1995). The inventor first asked if chaperones influenced conversion with PrP-res

that was not subjected to partial denaturation. Several chaperones produced reproducible, but very small increases in conversion (FIG. 5B and FIG. 5D). One, however, facilitated conversion at a high level (FIG. 5A and FIG. 5B). With GroEL, typically 25-30%, and occasionally 50-100%, of ^{35}S-PrP^C converted.

Notably GroEL not only reduced by 10-fold the quantity of PrP^{Sc} required for detectable conversion, but also increased by more than 10-fold the maximal levels of conversion attained, compared to reactions nucleated with the same preparation of untreated PrP^{Sc}, but no GroEL (FIG. 5D). These effects of GroEL were dose-dependent (FIG. 5C).

5.2.2.3   GROEL EFFECTS REQUIRE ATP, BUT NOT GROES

GroEL-promoted protein folding usually, but not always, requires the co-chaperone GroES and ATP (Hartl, 1996; Buchner, 1996). PrP conversion was not observed in the absence of ATP (FIG. 5E). Moreover, two point mutants of GroEL, which block release of substrate (D87K and 337/349; Kocisko et al., 1994) strongly reduced conversion (FIG. 5E). Surprisingly, however, the stimulating effects of GroEL on ^{35}S-PrP^C conversion were consistently eliminated by GroES (FIG. 5D). This inhibition was due to an effect of GroES on GroEL, rather than on PrP, because GroES did not inhibit the denaturant-promoted conversion of ^{35}S-PrP^C that occurs in the absence of GroEL.

5.2.2.4   POST-TRANSLATIONAL PRP MODIFICATIONS MODESTLY AFFECT CHAPERONE-PROMOTED CONVERSIONS

The inventor used a PrP mutant that lacks the glycosylphosphatidylinositol (GPI) anchor (PrP^{GPI-}; Edenhofer et al., 1996; Freeman and Morimoto, 1996) and accumulates in mono- and unglycosylated form (FIG. 5F, right), to determine if these natural modifications affect chaperone-mediated conversion. Again, of the various chaperones tested, GroEL was the only one that efficiently stimulated conversion in the presence of untreated PrP^{Sc} (FIG. 5F); and, once again, GroEL-promoted effects were ablated in the absence of ATP and inhibited by GroES (FIG. 5F). With this form of PrP, however, conversion was more efficient (typically 30-40%).

Moreover, conversion was also achieved with a combination of Hsp104, Hsp70, and Hsp40, albeit less consistently and less strongly than with GroEL (FIG. 5F). Results similar to those obtained with PrP^{GPI-}, were also obtained with unglycosylated $^{35}S\text{-}PrP^C$ purified from cells cultured with tunicamycin. Therefore, the ability of the chaperones to mediate the conversion of

5 $^{35}S\text{-}PrP^C$ to PrP-res was modestly facilitated by the absence of N-linked sugars or the GPI-anchor.

5.2.2.5 CONVERSION KINETICS REVEAL A TWO-STEP PROCESS

When $^{35}S\text{-}PrP^C$ converts to PrP-res, it becomes associated with PrP^{Sc}, which is a pelletable aggregate (Caughey *et al.*, 1995; Bessen *et al.*, 1997). To gain insight into the

10 chaperone-mediated conversion process, the inventor analyzed the kinetics of conversion, monitoring both protease-resistance and insolubility. GroEL promoted the acquisition of both of these signature features of PrP^{Sc} in $^{35}S\text{-}PrP$ (FIG. 6A and FIG. 6B). In reactions driven with untreated PrP^{Sc} and GroEL, protease resistance was acquired at a pace similar to that observed in reactions nucleated with partially-denatured PrP^{Sc}, in the absence of GroEL (FIG. 6A).

15 Moreover, in both sets of reactions, protease-resistant radioactivity was found only in pelletable material (FIG. 6C).

Surprisingly, however, when the rate at which $^{35}S\text{-}PrP$ became insoluble was examined, the chaperone-driven reaction showed very different kinetics than those driven by partially-

20 denatured PrP^{Sc}. No pelletable radioactivity was detected at two hours in reactions driven by partially-denatured PrP^{Sc} (FIG. 6A and FIG. 6B). In striking contrast, in chaperone-driven reactions, the conversion of PrP to a pelletable form was virtually complete in two hours. This occurred long before $^{35}S\text{-}PrP$ converted to its characteristic protease-resistant form (FIG. 6A and FIG. 6B). This pelleting of $^{35}S\text{-}PrP^C$ was almost certainly due to an association with pre-existing

25 PrP^{Sc}, because in parallel reactions with GroEL, but without PrP^{Sc}, most $^{35}S\text{-}PrP^C$ remained soluble (FIG. 6B).

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5.2.2.6 IN REACTIONS NUCLEATED WITH PARTIALLY-DENATURED PrP^{Sc}, HSP104 ALSO PROMOTES CONVERSION

Another chaperone was effective in reactions seeded with partially-denatured PrP^{Sc}. For these reactions, a milder denaturant, urea, was used because some chaperones are sensitive to inhibition by GdnHCl (Todd and Lorimor, 1995). Moreover, the lower basal rate of conversion obtained with urea (FIG. 7A, buffer) allowed the inventor to test the ability of other chaperones to either inhibit or stimulate conversion.

None inhibited (FIG. 7A). Several stimulated, but only to a small degree (FIG. 7A). Strikingly, under these conditions, in addition to GroEL, Hsp104 strongly stimulated conversion (FIG. 7A). With Hsp104, typically 20-30%, occasionally more than 50% of total ^{35}S-PrP^C converted. The stimulatory effects of Hsp104 required partial denaturation of PrP^{Sc}, with pre-treatments in 3-4 M urea being optimal (FIG. 7B).

5.2.2.7 FOLDED STATE OF PrP^{Sc} GOVERNS PROPERTIES OF CHAPERONE-PROMOTED CONVERSION

While some Hsp104 functions require ATP (Parsell and Lindquist, 1993; Schirmer et al., 1996), in these reactions nucleotide was somewhat stimulatory, but was not required (FIG. 7C). Furthermore, two ATPase-deficient Hsp104 mutants (KT218 and KT620; Pan et al., 1993) promoted ^{35}S-PrP^C conversion nearly as well as wild-type Hsp104 (FIG. 7C).

Remarkably, the use of partially-denatured PrP^{Sc} changed the character of conversions promoted by GroEL as well. These conversions lost ATP-dependence (FIG. 7D). Moreover, they became refractory to GroES inhibition (FIG. 7A). Thus, chaperone-mediated conversions are mechanistically distinct in reactions nucleated with partially-denatured PrP^{Sc}, and those nucleated by untreated PrP^{Sc}.

5.2.2.8 CHEMICAL CHAPERONES INHIBIT CONVERSION

The inventor also tested the effects of several small organic molecules (or chemical chaperones) known to affect protein folding: sucrose, glycerol, trehalose, DMSO and the

cyclodextrin compounds (Talzelt *et al.*, 1996; Welch and Brown , 1996; Yancey *et al.*, 1982). None of the compounds tested affected ^{35}S-PrP^C conversions in reactions without PrP^{Sc}, nor in reactions seeded with untreated PrP^{Sc}.

5   In reactions seeded with partially denatured PrP^{Sc}, DMSO had a complex dose-dependent effect, intermediate levels (1-3%) stimulated conversion 2-3 fold and higher levels (up to 30%) virtually eliminated conversion (FIG. 8). Glycerol (FIG. 8) and cyclodextrin compounds (α-,β-,γ-forms) had no effect. Sucrose and trehalose inhibited conversion. This inhibition was observed only at high concentrations, but is physiologically relevant because these osmolytes are known to accumulate to such levels *in vivo* under stressful conditions (Yancey *et al.*, 1982).

5.2.3 DISCUSSION

Recently, protein chaperones and small organic molecules have figured prominently among cellular factors speculated to influence conversion of PrP^C to PrP^{Sc} (Kenward *et al.*, 1996; Talzelt *et al.*, 1996; Telling *et al.*, 1995; Edenhofer *et al.*, 1996). In scrapie-infected cells, some of the same organic molecules the inventor tested have been shown to reduce the rate of PrP^{Sc} formation (Talzelt *et al.*, 1996). The inventor provides the first evidence that protein chaperones and small organic molecules can directly affect conformational transitions of PrP. The inventor's findings also provide the first direct demonstration that chaperone Hsp104 can alter the conformation state of another protein.

In studying the conversion of PrP^C to PrP-res, the inventor employed previously characterized chaperones from bacteria and the eukaryotic cytosol because protein chaperones have not yet been identified in compartments where PrP^C converts to PrP^{Sc}. Indeed, the site where conversion occurs is still unclear. WT PrP^C is thought to convert extracellularly, within endosomes, or in caveolae (Caughey and Raymond, 1991; Borchelt *et al.*, 1992; Vey *et al.*, 1996). Mutant PrP, proposed to model inherited TSEs, can acquire certain PrP^{Sc}-like properties spontaneously in the ER/Golgi complex (Daude *et al.*, 1997). Of the chaperones the inventor tested, only GroEL and Hsp104 affected conversion. The inventor's results indicate that such chaperone interactions *in vivo* are likely to be highly specific. Clearly, the elucidation of PrP

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chaperone interactions *in vivo* are of great import as they provide potential targets for therapeutic intervention.

The inventor's discoveries provide a unifying biochemical connection between mammalian TSEs (the so called "prion" diseases) and [PSI+], a novel genetic element in yeast (sometimes called a "yeast prion"; Wickner, 1994). The proposed "mammalian prion" determinant PrP^Sc, and the "yeast prion" determinant Sup35 are functionally unrelated and share no sequence identity. Moreso, [PSI+] produces a heritable change in metabolism rather than a lethal infection. However, both mammalian and yeast "prions" apparently share a common mode of transmission based upon self-propagating changes in protein conformation (Glover *et al.*, 1997; Chernoff *et al.*, 1995; Patino *et al.*, 1996).

Among yeast chaperones, the striking specificity of Hsp104 for PrP conversions, and its known *in vivo* specificity in regulating [PSI+] (Wickner , 1994; Glover *et al.*, 1997; Chernoff *et al.*, 1995; Patino *et al.*, 1996) suggest that conformations of PrP and Sup35 share an underlying biochemical similarity that allows for recognition by particular chaperones and prion-like conformational transitions. The present invention evidences the specific interactions of Hsp104 with PrP and Sup35 proteins using circular dichroism and ATP hydrolysis measurements.

The standard for testing the disease properties of PrP is to determine its protease resistance pattern. The protease resistant form is associated with disease. The inventor has shown that PrP when produced in yeast is protease resistant and that this protease resistant state depends upon the Hsp104 protein. Thus the protease-resistant character of PrP, which is the hallmark of its disease potential, is affected by manipulation of yeast cells. The inventor also shows that these same manipulations of yeast cells alter the folding state and protease resistance of a yeast amyloid protein. Together these results establish that manipulating yeast cells provides a general mechanism for studying factors that control the folding of amyloidogenic proteins. Amyloid proteins are important causative factors in many human diseases. Thus, the presently disclosed, inventive use of yeast cells provides an excellent system for testing and manipulating the folding state of amyloid proteins, which is useful in identifying therapeutic agents.

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<center>*   *   *</center>

All of the methods and apparatus disclosed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the methods and apparatus and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention.

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WHAT IS CLAIMED IS:

1.   A method of identifying a candidate substance that inhibits the aggregation of an aggregate-prone amyloid protein, comprising:

(a)   contacting a yeast cell that expresses an aggregate-prone amyloid protein with said candidate substance under conditions effective to allow aggregated amyloid formation; and

(b)   determining the ability of said candidate substance to inhibit the aggregation of the aggregate-prone amyloid protein.

2.   The method of claim 1, wherein the aggregate-prone amyloid protein comprises a Sup35 or URE3 polypeptide.

3.   The method of claim 1, wherein the aggregate-prone amyloid protein comprises a PrP or β-amyloid polypeptide.

4.   The method of claim 1, wherein the aggregate-prone amyloid protein is a chimeric protein.

5.   The method of claim 4, wherein the chimeric protein comprises at least the N-terminal domain of Sup35.

6.   The method of claim 4, wherein the chimeric protein comprises at least an aggregate forming domain of a mammalian amyloid polypeptide.

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7. The method of claim 4, wherein the chimeric protein comprises at least an aggregate forming domain of an aggregate-prone amyloid protein operably attached to a detectable marker protein.

8. The method of claim 7, wherein said marker protein is green fluorescent protein or luciferase.

9. The method of claim 7, wherein said marker protein is a drug-resistance marker protein.

10. The method of claim 7, wherein said marker protein is a hormone receptor.

11. The method of claim 10, wherein said hormone receptor is a glucocorticoid receptor.

12. The method of claim 6, wherein the mammalian amyloid polypeptide is PrP or β-amyloid.

13. The method of claim 12, wherein the chimeric protein comprises as least about amino acids 1-42 of β-amyloid protein.

14. The method of claim 4, wherein the chimeric protein comprises Sup35 in which the N-terminal domain has been replaced by amino acids 1-42 of β-amyloid protein.

15.   The method of claim 1, wherein any aggregation of the aggregate-prone amyloid protein is detected by the ability of the aggregated protein to bind Congo Red.

16.   The method of claim 1, wherein any aggregation of the aggregate-prone amyloid protein is detected by increased protease resistance of the aggregated protein.

17.   The method of claim 1, wherein the aggregate-prone amyloid protein is labeled.

18.   The method of claim 17, wherein the label is a radioactive isotope, a fluorophore, or a chromophore.

19.   The method of claim 18, wherein the label is ^{35}S.

20.   The method of claim 18, wherein the fluorophore comprises a green fluorescent protein polypeptide.

21.   The method of claim 1, wherein any aggregation is determined by the presence of a [PSI+] phenotype.

22.   The method of claim 1, wherein said yeast cell overexpresses Hsp104.

23.   A method of identifying a candidate substance for therapeutic activity against an amyloidogenic disease in an animal, said method comprising:

    (a)   contacting a yeast cell that expresses an aggregate-prone amyloid protein with said candidate substance under conditions effective to allow amyloid formation; and

    (b)   determining the ability of said candidate substance to inhibit aggregation of the aggregate-prone amyloid protein,

    wherein the ability to inhibit aggregation is indicative of therapeutic activity.

24.   The method of claim 23, wherein the aggregate-prone amyloid protein comprises a PrP, β-amyloid, Sup35, or URE3 polypeptide.

25.   The method of claim 23, wherein the protein is a chimeric protein.

26.   The method of claim 25, wherein the chimeric protein comprises a Sup35 polypeptide.

27.   The method of claim 25, wherein the chimeric protein comprises a mammalian amyloid polypeptide.

28.   The method of claim 27, wherein the mammalian amyloid polypeptide is PrP or β-amyloid.

29.   The method of claim 23, wherein any aggregation of the aggregate-prone amyloid protein is detected by the ability of the aggregation to bind Congo Red.

5   30.   The method of claim 23, wherein the aggregate-prone amyloid protein is labeled.

31.   The method of claim 30, wherein the label is a radioactive isotope, a fluorophore, or a chromophore.

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32.   The method of claim 31, wherein the label is ^{35}S.

15   33.   The method of claim 31, wherein the fluorophore comprises a green fluorescent protein polypeptide.

34.   The method of claim 23, wherein the aggregation of the aggregate-prone amyloid protein 20   is determined by the presence of a [PSI+] phenotype.

35.   The method of claim 23, wherein the disease is selected from the group consisting of Alzheimer's disease, scrapie, spongiform encephalopathy in a mammal, kuru, Creutzfeldt-Jakob 25   disease, Gestmann-Strausser-Scheinker disease, or fatal familial insomnia.

36.   The method of claim 35, wherein the mammal is bovine, feline, a mink, deer, elk, a mouse, a hamster, an ape, a monkey, or human.

ABSTRACT

The present invention provides a yeast cell based system for determining factors that control the folding of amyloid proteins of diverse origins. Further the present invention provides methods of using such a system to screen for reagents that affect amyloid formation, a process that is integral to several devastating human disease including Creutzfeld-Jacob disease (CJD), fatal familial insomnia (FFI), Gertsmann-Straussler-Scheinker (GSS) syndrome, and kuru. The system of the present invention provides a rapid screening system to quickly and cheaply identify reagents that affect the folding and aggregation properties of the target protein.

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FIG. 1A.

Individual / Combined

Sup35 + Aldolase

Sup35 + Hsp70

FIG. 1B.

Hsp104 + Aldolase

Hsp104 + IgM

FIG. 1C.

Low Salt pH 6.5 Sup35 + Hsp104

High Salt pH 7.5 Sup35 + Hsp104

FIG. 2A.

FIG. 2B.

FIG. 2C.

FIG. 2D.

FIG. 3 A.

FIG. 3 B.

FIG. 4 A. — aa 57-91 (peptide B)

FIG. 4 B. — aa 90-145 (peptide F)

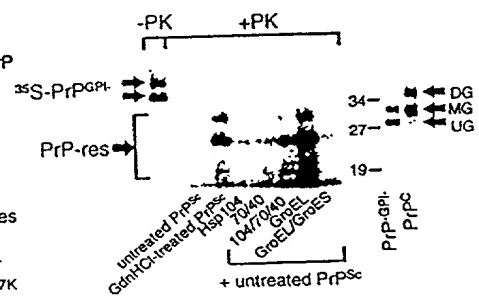FIG. 4 C. — aa 141-178 (peptide G)

FIG. 4 D. — aa 178-231 (peptide J)

FIG. 5 A

FIG. 5 B

FIG. 5 C

FIG. 5 D

FIG. 5 E

FIG. 5 F

FIG. 6 A

FIG. 6 B

time (hr)

- ○ — buffer
- △ — GroEL alone
- ▲ — untreated PrP^{Sc} + GroEL
- □ — untreated PrP^{Sc} alone
- ■ — GdnHCl-treated PrP^{Sc}

FIG. 6 C

FIG. 7 A

+ partially-denatured PrPSc

% conversion

buffer
BSA
GroES
Hsp2b
Hsp40
GroEL
GroEL:GroES
Hsp70
70→40
Hsp90
90→70→40
Hsp104
104+70→40

FIG. 7 B

PrPSc pretreatment
Urea [M]: 0 1 2 3 4 5

control

GroEL   +PK

Hsp104

FIG. 7 C

PrPSc pretreatment
Urea (4M)

Hsp104 WT
(-ATP)

+PK

Hsp104 WT
(-ATP)

Hsp104 KT218
(-ATP)

0 10 30 100 300 3000   0 10 30 100 300 3000   [Hsp104] (nM)

FIG. 7 D

-PK

34—
27—   35S-PrPC

+PK

34—
27—   PrP-res

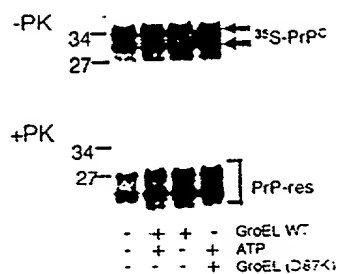- + + - GroEL WT
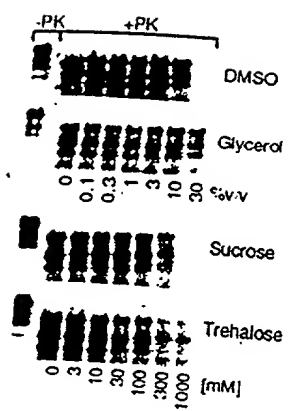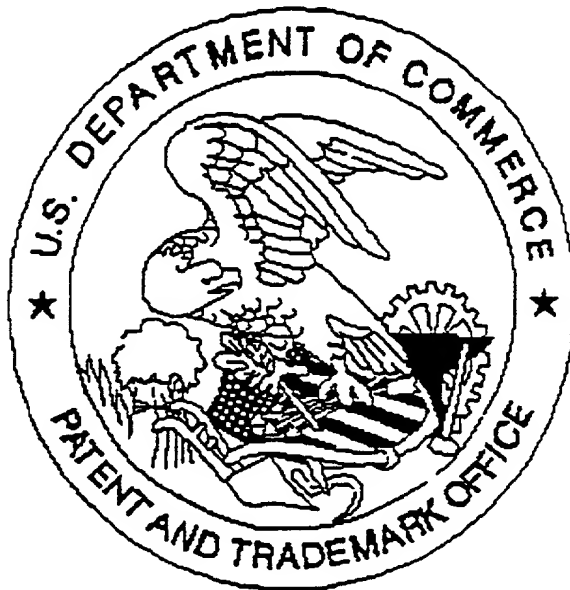- + - + ATP
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FIG. 8

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